

Package ‘hutan’

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Title A Collection of Tools for Phylogenetic Tree Manipulation

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Description A collection of tools for phylogenetic tree manipulation. It is named after the Indonesian word for forest.

Depends R (>= 3.1.0)

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LazyData true

Collate 'utility_functions.R'
'hutan.R'
'siphonophore_constraint.R'
'siphonophore_ml.R'

Imports ape (>= 3.3),
tidyverse

Suggests testthat,
roxygen2,
knitr

VignetteBuilder knitr

RoxygenNote 6.0.1

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ancestral_edges	<i>For a node in a tree, get a vector of the edges between the node and the root</i>
-----------------	--

Description

For a node in a tree, get a vector of the edges between the node and the root

Usage

ancestral_edges(phy, node)

Arguments

phy	A phylo object
node	A node number

Value

A vector of edge numbers

are_bipartitions_compatible	<i>Check if two bipartitions drawn from trees with the same tips are compatible with eachother. Each bipartition is defined as a vector of the names of the tips on one side of the bipartition.</i>
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Description

Check if two bipartitions drawn from trees with the same tips are compatible with eachother. Each bipartition is defined as a vector of the names of the tips on one side of the bipartition.

Usage

are_bipartitions_compatible(bi1, bi2, phy)

Arguments

bi1	The first bipartition.
bi2	The second bipartition.
phy	A phylo object describing a tree that includes all tips under investigation. This is used to infer the other half of each bipartition.

Value

TRUE if bi1 is compatible with bi2, otherwise FALSE.

bipartition_for_edge	<i>Get a bipartition, described as a vector of tip numbers, from a specified tree and edge number.</i>
----------------------	--

Description

Get a bipartition, described as a vector of tip numbers, from a specified tree and edge number.

Usage

```
bipartition_for_edge(phy, edge)
```

Arguments

phy	A phylo object that specifies the tree.
edge	The number of the edge that defines the bipartition.

Value

A vector of tip nodes (specified by numbers) that define one half of the bipartition (the other half is the set of tip nodes that are not in this vector).

bipartition_for_edge_by_label	<i>Get a bipartition, described as a vector of tip labels, from a specified tree and edge number.</i>
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Description

Get a bipartition, described as a vector of tip labels, from a specified tree and edge number.

Usage

```
bipartition_for_edge_by_label(edge, phy)
```

Arguments

edge	The number of the edge that defines the bipartition.
phy	A phylo object that specifies the tree.

Value

A vector of tip nodes (specified by labels) that define one half of the bipartition (the other half is the set of tip nodes that are not in this vector).

compatible_edges	<i>Identify the edges in one phylo object that are compatible with the edges in another phylo object. Requires the same tip labels for each tree.</i>
------------------	---

Description

Identify the edges in one phylo object that are compatible with the edges in another phylo object. Requires the same tip labels for each tree.

Usage

```
compatible_edges(phy1, phy2)
```

Arguments

phy1	The tree under consideration
phy2	The tree to be compared to

Value

A boolean vector corresponding to the edges in phy1. Each element is FALSE if the edge is incompatible with phy2, or TRUE if compatible.

connecting_edges	<i>For two nodes in a tree, get a vector of the edges that connect them</i>
------------------	---

Description

For two nodes in a tree, get a vector of the edges that connect them

Usage

```
connecting_edges(phy, node_a, node_b)
```

Arguments

phy	A phylo object
node_a	Number of the first node
node_b	Number of the second node

Value

A vector of edge numbers

cut_tree	<i>Cuts a single tree on the branch subtending a specified node</i>
----------	---

Description

Cuts a single tree on the branch subtending a specified node

Usage

```
cut_tree(phy, x)
```

Arguments

phy	The tree to be cut, as an ape phylo object
x	An internal node number. The tree phy will be cut on the branch that subtends this nodes.

Value

A list of phylo objects that are the subtrees

decompose_tree	<i>Decomposes a single tree into a series of subtrees designated by internal node numbers</i>
----------------	---

Description

Decomposes a single tree into a series of subtrees designated by internal node numbers

Usage

```
decompose_tree(phy, x)
```

Arguments

phy	The tree to be decomposed, as an ape phylo object
x	A vector of internal node numbers. The tree phy will be cut on each branch that subtends each of these nodes.

Value

A list of phylo objects

descendants	<i>Get all the descendants of a given node in a tree.</i>
-------------	---

Description

Get all the descendants of a given node in a tree.

Usage

```
descendants(phy, a, keep_node = FALSE)
```

Arguments

phy	A phylo object that specifies the tree.
a	The number of a node in phy.
keep_node	If FALSE, do not include a in the result.

Value

A vector of nodes (specified by number) that are descendants of a. Includes internal and tip nodes.

difference_from_calibrated	<i>Assesses how much phy deviates from an ultrametric tree</i>
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Description

Assesses how much phy deviates from an ultrametric tree

Usage

```
difference_from_calibrated(phy, model = "discrete", ...)
```

Arguments

phy	A phylo object
model	The model used for fitting. "discrete" is used by default for speed
...	Additional chronos arguments

Value

The sum of absolute changes in branch length required to make an ape::chronos time calibrated tree, normalized by the total branch length of the calibrated tree. The higher the value, the more the tree deviates from the calibrated tree.

distance_from_tip	<i>For each node in the tree (including internal nodes and tips) get the shortest distance to a descendant node. Values for tip nodes should be 0.</i>
-------------------	--

Description

For each node in the tree (including internal nodes and tips) get the shortest distance to a descendant node. Values for tip nodes should be 0.

Usage

```
distance_from_tip(phy)
```

Arguments

phy	A phylo object
-----	----------------

Value

A vector with elements corresponding to each node

extend_terminal_branches	<i>Extends each terminal branch by specified length</i>
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Description

Extends each terminal branch by specified length

Usage

```
extend_terminal_branches(phy, x)
```

Arguments

phy	A phylogeny in ape::phylo format
x	Amount to extend each branch by

Value

A phylogeny in ape::phylo format

flip_bipartition	<i>Given a tree and a bipartition, described as a vector of tip labels on one side of of the bipartition, return the same bipartition but defined by the tip labels on the other side of the bipartition.</i>
------------------	---

Description

Given a tree and a bipartition, described as a vector of tip labels on one side of of the bipartition, return the same bipartition but defined by the tip labels on the other side of the bipartition.

Usage

```
flip_bipartition(phy, bi)
```

Arguments

phy	A phylo object that specifies the tree.
bi	The bipartition.

Value

A vector of tip nodes (specified by labels) that define one half of the bipartition (the other half is the set of tip nodes that are provided as bi).

get_bipartitions	<i>Get a list of all the bipartitions in a tree.</i>
------------------	--

Description

Get a list of all the bipartitions in a tree.

Usage

```
get_bipartitions(phy)
```

Arguments

phy	A phylo object that specifies the tree.
-----	---

Value

A list of bipartitions for the tree. The order of the list corresponds to the edges in phy\$edge. Bipartitions are specified as a vector of the tip labels that make up one half of the bipartition.

get_corresponding_nodes

Given two trees phy1 and phy2 with the same topology and tip labels, get a vector that indicates which node numbers in phy2 correspond to the nodes in phy1

Description

Given two trees phy1 and phy2 with the same topology and tip labels, get a vector that indicates which node numbers in phy2 correspond to the nodes in phy1

Usage

```
get_corresponding_nodes(phy1, phy2)
```

Arguments

phy1	A phylo object
phy2	A phylo object

Value

A numeric vector in the order of nodes in phy1, providing corresponding node numbers from phy2

hutan

hutan: A collection of tools for phylogenetic tree manipulation.

Description

The hutan package provides functions for common phylogenetic tree manipulation tasks, and uses these facilitate some more specialized tasks. It is named after the Indonesian word for forest.

is_compatible_with_set

Check if bipartition bi is compatible with the bipartitions in bi_list. Each bipartition is defined as a vector of the names of the tips on one side of the bipartition.

Description

Check if bipartition bi is compatible with the bipartitions in bi_list. Each bipartition is defined as a vector of the names of the tips on one side of the bipartition.

Usage

```
is_compatible_with_set(bi, bi_list, phy)
```

Arguments

bi	The query bipartition.
bi_list	A list of the bipartitions to be compared against.
phy	A phylo object describing a tree that includes all tips under investigation. This is used to infer the other half of each bipartition.

Value

TRUE if bi is compatible with all bipartition in bi_list, otherwise FALSE.

is_monophyletic	<i>Test if a set of tips, specified as a vector of tip labels, forms a monophyletic group in a given tree. The test is unrooted, i.e. the group can span the root.</i>
-----------------	--

Description

Test if a set of tips, specified as a vector of tip labels, forms a monophyletic group in a given tree. The test is unrooted, i.e. the group can span the root.

Usage

```
is_monophyletic(phy, x)
```

Arguments

phy	The tree under consideration
x	A vector of the labels of the tips in question

Value

A boolean, TRUE if the tips form a monophyletic group.

safe.drop.tip	<i>Drops specified tips from a phylogeny. Like ape's drop.tip(), but it works when only a single tip is to be retained.</i>
---------------	---

Description

Drops specified tips from a phylogeny. Like ape's drop.tip(), but it works when only a single tip is to be retained.

Usage

```
safe.drop.tip(phy, tip)
```

Arguments

phy	The tree, as an ape phylo object
tip	A vector of tip numbers to be removed.

Value

The reduced tree, as a phylo object

siphonophore_constraint

Siphonophores constraint phylogeny.

Description

An unresolved phylogeny that constrains the group Agalmatidae sensu stricto + Bargmannia to be monophyletic, corresponding to the published SOWH test

Usage

siphonophore_constraint

Format

An ape phylo object

Source

<http://dx.doi.org/10.1080/10635150500354837>

siphonophore_ml

Siphonophores phylogeny.

Description

A maximum likelihood phylogeny of siphonophores

Usage

siphonophore_ml

Format

An ape phylo object

Source

<http://dx.doi.org/10.1080/10635150500354837>

slide_root_edges	<i>Repartitions lengths along edges that descend from root node so that they are equal. Useful after rooting operations that result in branches with 0 length</i>
------------------	---

Description

Repartitions lengths along edges that descend from root node so that they are equal. Useful after rooting operations that result in branches with 0 length

Usage

```
slide_root_edges(phy)
```

Arguments

phy	A phylo object
-----	----------------

Value

A phylo object with modified edge lengths

tips	<i>Get tips and labels of a phylo object.</i>
------	---

Description

Get tips and labels of a phylo object.

Usage

```
tips(phy)
```

Arguments

phy	A phylo object.
-----	-----------------

Value

A vector of all the tips, annotated with their names

tip_descendants	<i>Get all the tips that are descendants of a given node in a tree.</i>
-----------------	---

Description

Get all the tips that are descendants of a given node in a tree.

Usage

```
tip_descendants(phy, a)
```

Arguments

phy	A phylo object that specifies the tree.
a	The number of a node in phy.

Value

A vector of tip nodes (specified by number) that are descendants of a. If a is a tip, it is the sole element of this vector.

zero_constrained	<i>Generates the "zero-constrained" tree described by Susko 2014 (http://dx.doi.org/10.1093/molbev/msu039)</i>
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Description

Generates the "zero-constrained" tree described by Susko 2014 (<http://dx.doi.org/10.1093/molbev/msu039>)

Usage

```
zero_constrained(phy_resolved, phy_constraint, epsilon = 1e-06)
```

Arguments

phy_resolved	A fully resolved phylogeny stored as a phylo object, e.g. an ML tree.
phy_constraint	A partially resolved constraint tree.
epsilon	The value to replace the branch length with

Value

A phylo object containing a tree that is the same as phy_resolved, except that the length of edges that are incompatible with phy_constraint are replaced with epsilon.

Examples

```
data( siphonophore_ml )
data( siphonophore_constraint )
zc <- zero_constrained( siphonophore_ml, siphonophore_constraint )
```

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